

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Eaton, Dan L.
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

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10      (iii) NUMBER OF SEQUENCES: 21

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(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/430035
(B) FILING DATE: 27-Apr-1995
(C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 03-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Winter, Daryl B.
(B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: P0871P2D2

(ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 415/225-1249
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
-16 -15 -10 -5
Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
1 5 10
15 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
15 20 25 26

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50
CACCTCTCCT CATCTAAGAA TTG CTC CTC GTG GTC ATG CTT 91
Leu Leu Leu Val Val Met Leu
-16 -15 -10
35 CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130
Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro
-5 1
40 CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169
Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg
5 10 15
45 GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210
Asp Ser His Val Leu His Ser Arg Leu
20 25 26
CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260
50 GACACCATCA CTCCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310
TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360

ACAGCCCGCA TTATAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTAGACGAG AGCTTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50
TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100
GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150
TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200
GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250
CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300
AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350
ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
-21 -20 -15 -10
Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
-5 1 5
Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
10 15 20
Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
25 30 35
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40 45 50

	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	
	55					60					65					
5	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	
	70					75					80					
	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	
	85					90					95					
10	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	
	100					105					110					
	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	
	115					120					125					
15	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	
	130					135					140					
	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	
20	145					150					155					
	Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu	
	160					165					170					
25	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	
	175					180					185					
	Ala	Arg	Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	
	190					195					200					
30	Arg	Ala	Lys	Ile	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	
	205					210					215					
	Asp	Gln	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	
35	220					225					230					
	Gly	Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	
	235					240					245					
40	Ala	Pro	Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	
	250					255					260					
	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	
	265					270					275					
45	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr	
	280					285					290					
	Pro	Val	Val	Gln	Leu	His	Pro	Leu	Leu	Pro	Asp	Pro	Ser	Ala	Pro	
50	295					300					305					
	Thr	Pro	Thr	Pro	Thr	Ser	Pro	Leu	Leu	Asn	Thr	Ser	Tyr	Thr	His	

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Ser Gln Asn Leu Ser Gln Glu Gly
325 330 332

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1798 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGTCTTCCT ACCCATCTGC TCCCCAGAGG GCTGCCTGCT GTGCACTTGG 50

GTCCTGGAGC CCTTCTCCAC CCGGATAGAT TCCTCACCCCT TGGCCCGCCT 100

20

TTGCCCCACC CTACTCTGCC CAGAAGTGCA AGAGCCTAAG CCGCCTCCAT 150

GGCCCCAGGA AGGATTCAGG GGAGAGGCC CAAACAGGGA GCCACGCCAG 200

25

CCAGACACCC CGGCCAGA ATG GAG CTG ACT GAA TTG CTC CTC 242

Met Glu Leu Thr Glu Leu Leu Leu

-21 -20

-15

GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 281

Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser

-10

-5

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AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 320

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser

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AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 359

Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu

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25

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AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 398

Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val

30

35

CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 437

Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys

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ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA 476

Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly

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	GCA	GTG	ACC	CTT	CTG	CTG	GAG	GGA	GTG	ATG	GCA	GCA	CGG	515
	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	
					70					75				
5	GGA	CAA	CTG	GGA	CCC	ACT	TGC	CTC	TCA	TCC	CTC	CTG	GGG	554
	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	
		80					85					90		
10	CAG	CTT	TCT	GGA	CAG	GTC	CGT	CTC	CTC	CTT	GGG	GCC	CTG	593
	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	
				95					100					
15	CAG	AGC	CTC	CTT	GGA	ACC	CAG	CTT	CCT	CCA	CAG	GGC	AGG	632
	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	
	105					110					115			
20	ACC	ACA	GCT	CAC	AAG	GAT	CCC	AAT	GCC	ATC	TTC	CTG	AGC	671
	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	
			120					125					130	
25	TTC	CAA	CAC	CTG	CTC	CGA	GGA	AAG	GTG	CGT	TTC	CTG	ATG	710
	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	
					135					140				
30	CTT	GTA	GGA	GGG	TCC	ACC	CTC	TGC	GTC	AGG	CGG	GCC	CCA	749
	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	
		145					150					155		
35	CCC	ACC	ACA	GCT	GTC	CCC	AGC	AGA	ACC	TCT	CTA	GTC	CTC	788
	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	
				160					165					
40	ACA	CTG	AAC	GAG	CTC	CCA	AAC	AGG	ACT	TCT	GGA	TTG	TTG	827
	Thr	Leu	Asn	Glu	Leu	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	
	170					175					180			
45	GAG	ACA	AAC	TTC	ACT	GCC	TCA	GCC	AGA	ACT	ACT	GGC	TCT	866
	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser	
			185					190					195	
50	GGG	CTT	CTG	AAG	TGG	CAG	CAG	GGA	TTC	AGA	GCC	AAG	ATT	905
	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	
				200						205				
55	CCT	GGT	CTG	CTG	AAC	CAA	ACC	TCC	AGG	TCC	CTG	GAC	CAA	944
	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	
		210					215					220		
60	ATC	CCC	GGA	TAC	CTG	AAC	AGG	ATA	CAC	GAA	CTC	TTG	AAT	983
	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	
				225					230					

	GGA	ACT	CGT	GGA	CTC	TTT	CCT	GGA	CCC	TCA	CGC	AGG	ACC	1022
	Gly	Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	
	235					240					245			
5	CTA	GGA	GCC	CCG	GAC	ATT	TCC	TCA	GGA	ACA	TCA	GAC	ACA	1061
	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp	Thr	
		250					255					260		
10	GGC	TCC	CTG	CCA	CCC	AAC	CTC	CAG	CCT	GGA	TAT	TCT	CCT	1100
	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	Pro	
					265					270				
15	TCC	CCA	ACC	CAT	CCT	CCT	ACT	GGA	CAG	TAT	ACG	CTC	TTC	1139
	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	
		275					280					285		
20	CCT	CTT	CCA	CCC	ACC	TTG	CCC	ACC	CCT	GTG	GTC	CAG	CTC	1178
	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr	Pro	Val	Val	Gln	Leu	
				290					295					
	CAC	CCC	CTG	CTT	CCT	GAC	CCT	TCT	GCT	CCA	ACG	CCC	ACC	1217
	His	Pro	Leu	Leu	Pro	Asp	Pro	Ser	Ala	Pro	Thr	Pro	Thr	
	300					305					310			
25	CCT	ACC	AGC	CCT	CTT	CTA	AAC	ACA	TCC	TAC	ACC	CAC	TCC	1256
	Pro	Thr	Ser	Pro	Leu	Leu	Asn	Thr	Ser	Tyr	Thr	His	Ser	
			315					320					325	
30	CAG	AAT	CTG	TCT	CAG	GAA	GGG	TAA	GGTTCTCAGA	CACTGCCGAC				1300
	Gln	Asn	Leu	Ser	Gln	Glu	Gly							
					330		332							
35	ATCAGCATTG	TCTCATGTAC	AGCTCCCTTC	CCTGCAGGGC	GCCCCTGGGA									1350
	GACAACTGGA	CAAGATTTC	TACTTTCTCC	TGAAACCCAA	AGCCCTGGTA									1400
	AAAGGGATAC	ACAGGACTGA	AAAGGGAATC	ATTTTTCAC	GTACATTATA									1450
40	AACCTTCAGA	AGCTATTTTT	TTAAGCTATC	AGCAATACTC	ATCAGAGCAG									1500
	CTAGCTCTTT	GGTCTATTTT	CTGCAGAAAT	TTGCAACTCA	CTGATTCTCT									1550
	ACATGCTCTT	TTTCTGTGAT	AACTCTGCAA	AGGCCTGGGC	TGGCCTGGCA									1600
45	GTTGAACAGA	GGGAGAGACT	AACCTTGAGT	CAGAAAACAG	AGAAAGGGTA									1650
	ATTTCCCTTG	CTTCAAATTC	AAGGCCTTCC	AACGCCCCCA	TCCCCTTTAC									1700
	TATCATTCTC	AGTGGGACTC	TGATCCCAT	TTCTTAACAG	ATCTTTACTC									1750
50	TTGAGAAATG	AATAAGCTTT	CTCTCAGAAA	AAAAAAAAAA	AAAAAAAAAA									1798

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1798 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT TTTTTTTTTT TCTGAGAGAA AGCTTATTCA TTTCTCAAGA 50
GTAAAGATCT GTTAAGAATA TGGGATCAGA GTCCCACTGA GAATGATAGT 100
AAAGGGGATG GGGGCGTTGG AAGGCCTTGA ATTTGAAGCA AAGGAAATTA 150
CCCTTTCTCT GTTTTCTGAC TCAAGGTTAG TCTCTCCCTC TGTTCAACTG 200
CCAGGCCAGC CCAGGCCTTT GCAGAGTTAT CACAGAAAAA GAGCATGTAG 250
AGAATCAGTG AGTTGCAAAT TTCTGCAGAA AATAGACCAA AGAGCTAGCT 300
GCTCTGATGA GTATTGCTGA TAGCTTAAAA AAATAGCTTC TGAAGGTTTA 350
TAATGTACAG TGAAAAATGA TTCCCTTTTC AGTCCTGTGT ATCCCTTTTA 400
CCAGGGCTTT GGGTTTCAGG AGAAAGTAGG AAATCTTGTC CAGTTGTCTC 450
CCAGGGGCGC CCTGCAGGGA AGGGAGCTGT ACATGAGACA ATGCTGATGT 500
CGGCAGTGTC TGAGAACCTT ACCCTTCCTG AGACAGATTC TGGGAGTGGG 550
TGTAGGATGT GTTTAGAAGA GGGCTGGTAG GGGTGGGCGT TGGAGCAGAA 600
GGGTCAGGAA GCAGGGGGTG GAGCTGGACC ACAGGGGTGG GCAAGGTGGG 650
TGGAAGAGGG AAGAGCGTAT ACTGTCCAGT AGGAGGATGG GTTGGGGAAG 700
GAGAATATCC AGGCTGGAGG TTGGGTGGCA GGGAGCCTGT GTCTGATGTT 750
CCTGAGGAAA TGTCCGGGGC TCCTAGGGTC CTGCGTGAGG GTCCAGGAAA 800
GAGTCCACGA GTTCCATTCA AGAGTTCGTG TATCCTGTTC AGGTATCCGG 850
GGATTTGGTC CAGGGACCTG GAGGTTTGGT TCAGCAGACC AGGAATCTTG 900
GCTCTGAATC CCTGCTGCCA CTTCAGAAGC CCAGAGCCAG TAGTTCTGGC 950
TGAGGCAGTG AAGTTTGTCT CCAACAATCC AGAAGTCCTG TTTGGGAGCT 1000
CGTTCAGTGT GAGGACTAGA GAGGTTCTGC TGGGGACAGC TGTGGTGGGT 1050

GGGGCCCCGCC TGACGCAGAG GGTGGACCCT CCTACAAGCA TCAGGAAACG 1100
 CACCTTTCCT CGGAGCAGGT GTTGAAGCT CAGGAAGATG GCATTGGGAT 1150
 5 CCTTGTGAGC TGTGGTCCTG CCCTGTGGAG GAAGCTGGGT TCCAAGGAGG 1200
 CTCTGCAGGG CCCCAAGGAG GAGACGGACC TGTCCAGAAA GCTGCCCCAG 1250
 10 GAGGGATGAG AGGCAAGTGG GTCCCAGTTG TCCCCGTGCT GCCATCACTC 1300
 CCTCCAGCAG AAGGGTCACT GCTCCCAGAA TGTCTGTGC CTTGGTCTCC 1350
 TCCATCTGGG TTTTCCATTC TCCCAAGCTA AAGTCCACAG CAGGCAGCAG 1400
 15 GACAGGTGTA GGCAAAGGGT GAACCTCTGG GCACTGGCTC AGTCTGCTGT 1450
 GAAGGACATG GGAGTCACGA AGCAGTTTAC TGAGGACTCG GAGGTCACAA 1500
 GCAGGAGGAG CCGGGCTGGA CAGCGTTAGC CTTGCAGTTA GGAGAAGCAT 1550
 20 GACCACGAGG AGCAATTCAG TCAGCTCCAT TCTGGCCGGG GTGTCTGGCT 1600
 GCGTGGCTC CCTGTTTGGG GCCTCTCCCC TGAATCCTTC CTGGGGCCAT 1650
 25 GGAGGCGGCT TAGGCTCTTG CACTTCTGGG CAGAGTAGGG TGGGGCAAAG 1700
 GCGGGCCAAG GGTGAGGAAT CTATCCGGGT GGAGAAGGGC TCCAGGACCC 1750
 AAGTGCACAG CAGGCAGCCC TCTGGGGAGC AGATGGGTAG GAAGACGC 1798

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

40 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser
 1 5 10 15
 Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro
 20 25 30
 45 Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu
 35 40 45
 Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys
 50 50 55 60
 Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe

	65	70	75
	Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val		
	80	85	90
5	Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln		
	95	100	105
10	Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu		
	110	115	120
	His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu		
	125	130	135
15	Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp		
	140	145	150
	Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe		
	155	160	165
20	Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu		
	170	175	180
25	Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg		
	185	190	193

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 25 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

35	Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
	1 5 10 15
40	Leu Arg Asp Asp His Val Leu His Gly Arg
	20 25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 26 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

50	Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
	1 5 10 15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu
20 25 26

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15
Leu Arg Asp Asp Xaa Val Leu His Gly Arg Leu
20 25 26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15
Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCNGCNCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

NCCRTGNARN ACRTGRTCRT C 21

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

TGACCACGTT CAGCACGGC 69

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

5

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50
CGACCACGTC CATCACGGC 69

10 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: Amino Acid

15

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

20

Pro Arg Leu Leu Asn Lys Leu Leu Arg
1 5 9

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 69 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

35

CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 37 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGTCTGCCG TGAAGGACAT GG 22

10